

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT: Harada, John

Lotan, Tamar

Ohto, Masa-aki

Goldberg, Robert B.

Fischer, Robert L.

Bui, Anhthu

Kwong, Raymond

## (ii) TITLE OF INVENTION: Leafy Cotyledon1 Genes and Their Uses

## (iii) NUMBER OF SEQUENCES: 18

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend and Crew LLP

(B) STREET: Two Embarcadero Center, Eighth Floor

(C) CITY: San Francisco

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94111-3834

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/804,534

(B) FILING DATE: 21-FEB-1997

(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bastian, Kevin L.

(B) REGISTRATION NUMBER: 34,774

(C) REFERENCE/DOCKET NUMBER: 023070-077600US

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 576-0200

(B) TELEFAX: (415) 576-0300

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..627  
 (D) OTHER INFORMATION: /product= "LEC1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG ACC AGC TCA GTC ATA GTA GCC GGC GCC GGT GAC AAG AAC AAT GGT  
 48

Met Thr Ser Ser Val Ile Val Ala Gly Ala Gly Asp Lys Asn Asn Gly  
           1          5          10          15

ATC GTG GTC CAG CAG CAA CCA CCA TGT GTG GCT CGT GAG CAA GAC CAA  
 96

Ile Val Val Gln Gln Gln Pro Pro Cys Val Ala Arg Glu Gln Asp Gln  
                   20          25          30

TAC ATG CCA ATC GCA AAC GTC ATA AGA ATC ATG CGT AAA ACC TTA CCG  
 144

Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Thr Leu Pro  
           35          40          45

TCT CAC GCC AAA ATC TCT GAC GAC GCC AAA GAA ACG ATT CAA GAA TGT  
 192

Ser His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys  
           50          55          60

GTC TCC GAG TAC ATC AGC TTC GTG ACC GGT GAA GCC AAC GAG CGT TGC  
 240

Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala Asn Glu Arg Cys  
           65          70          75          80

CAA CGT GAG CAA CGT AAG ACC ATA ACT GCT GAA GAT ATC CTT TGG GCT  
 288

Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Ile Leu Trp Ala  
           85          90          95

ATG AGC AAG CTT GGG TTC GAT AAC TAC GTG GAC CCC CTC ACC GTG TTC  
 336

Met Ser Lys Leu Gly Phe Asp Asn Tyr Val Asp Pro Leu Thr Val Phe  
           100          105          110

ATT AAC CGG TAC CGT GAG ATA GAG ACC GAT CGT GGT TCT GCA CTT AGA  
384

Ile Asn Arg Tyr Arg Glu Ile Glu Thr Asp Arg Gly Ser Ala Leu Arg  
115 120 125

GGT GAG CCA CCG TCG TTG AGA CAA ACC TAT GGA GGA AAT GGT ATT GGG  
432

Gly Glu Pro Pro Ser Leu Arg Gln Thr Tyr Gly Gly Asn Gly Ile Gly  
130 135 140

TTT CAC GGC CCA TCT CAT GGC CTA CCT CCT CCG GGT CCT TAT GGT TAT  
480

Phe His Gly Pro Ser His Gly Leu Pro Pro Pro Gly Pro Tyr Gly Tyr  
145 150 155 160

GGT ATG TTG GAC CAA TCC ATG GTT ATG GGA GGT GGT CGG TAC TAC CAA  
528

Gly Met Leu Asp Gln Ser Met Val Met Gly Gly Gly Arg Tyr Tyr Gln  
165 170 175

AAC GGG TCG TCG GGT CAA GAT GAA TCC AGT GTT GGT GGT GGC TCT TCG  
576

Asn Gly Ser Ser Gly Gln Asp Glu Ser Ser Val Gly Gly Gly Ser Ser  
180 185 190

TCT TCC ATT AAC GGA ATG CCG GCT TTT GAC CAT TAT GGT CAG TAT AAG  
624

Ser Ser Ile Asn Gly Met Pro Ala Phe Asp His Tyr Gly Gln Tyr Lys  
195 200 205

TGA

627

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Ser Ser Val Ile Val Ala Gly Ala Gly Asp Lys Asn Asn Gly  
1 5 10 15

Ile Val Val Gln Gln Gln Pro Pro Cys Val Ala Arg Glu Gln Asp Gln  
20 25 30

Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Thr Leu Pro  
 35 40 45

Ser His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys  
 50 55 60

Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala Asn Glu Arg Cys  
 65 70 75 80

Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Ile Leu Trp Ala  
 85 90 95

Met Ser Lys Leu Gly Phe Asp Asn Tyr Val Asp Pro Leu Thr Val Phe  
 100 105 110

Ile Asn Arg Tyr Arg Glu Ile Glu Thr Asp Arg Gly Ser Ala Leu Arg  
 115 120 125

Gly Glu Pro Pro Ser Leu Arg Gln Thr Tyr Gly Gly Asn Gly Ile Gly  
 130 135 140

Phe His Gly Pro Ser His Gly Leu Pro Pro Pro Gly Pro Tyr Gly Tyr  
 145 150 155 160

Gly Met Leu Asp Gln Ser Met Val Met Gly Gly Arg Tyr Tyr Gln  
 165 170 175

Asn Gly Ser Ser Gly Gln Asp Glu Ser Ser Val Gly Gly Ser Ser  
 180 185 190

Ser Ser Ile Asn Gly Met Pro Ala Phe Asp His Tyr Gly Gln Tyr Lys  
 195 200 205

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGATCCAAAA CAGGTCATGG ACTGGGCCGT AAACCTATC CAAAATTCTT CATGTTTTTC 60  
 CATCTTTCAA AAATCTTTAT CCACCATTC ATTACTAGGG TGTGGTTTT ATTTTATTG 120  
 TTGATTAATT ATGTATTAGA AAATGTAAAG CAATATTCAA TTGTAACATG CATCATCTAA 180

CACCAATATC TTGTACTAAC CTTTGTAAAT TTTCCTATAA ACATTTTAAA AGGCTAATTT 240  
 AAATAAAAAAT TACAATAAAC GTGATAACTC ACTTTCGTAA CGCATATTTA TTCAAAATATA 300  
 CCAAAATTTA CCATTTTAAG TAAGAGAATC TTTTAAAAAT TAATTTTCAA TTTCATTAAT 360  
 TAAGAAACAA AGAATTTACT GAAACCTATA TTTTATTAAA TTTAATAAAA ATATATGACT 420  
 AAAATAACGT CACGTGAATC TTTCTCAGCC GTTCGATAAT CGAATACTTT ATTGACTAAG 480  
 TATTTATTTA GAAAATTTTA AACAACACTT AATTTCTAGA AACAAAGAGA GCCTCATATG 540  
 TATAAAAATC TTCTTCTTAT CTTTCTTTCT TTCTTAATAG TCTTTATTTT TACTTAATTA 600  
 CTTTGGTAAT TTGTGAAAAA CACAACCAAT GAGAGAAGAG CAGTTTGACT GGCCACATAG 660  
 CCAATGAGAC AAGCCAATGG GAAAGAGATA TAGAGACCTC GTAAGAACCG CTCCTTTGCC 720  
 ATTTGTATCA TCTCTCTATA AAACCACTCA ACCATCAACC TNTCTTTGCA TGCAACAAAT 780  
 CACTCAAATA ATTATTTTAT AAAGAACAAA AAAAAAAGA CGGCAGAGAA ACAATGGAAC 840  
 GTGGAGCTCC CTTCTCTCAC TATCAGCTAC CCAAATCCAT CTCTGGTAAT CTAAGTGGCT 900  
 ATTTGTATAC AGTATATACT TGCCTCCATG TATATTTATA TTCTCGTGAA AAATTGGAGA 960  
 CATGCTTTAT GAATTTTATG AGACTTTGCA ACAACGAACG AGATGCTTTC TCTCTAGAAA 1020  
 TTTAAATTTA GATTTGTGAA GGTTTGGGA ATGGCCCGGA GAAGACGATT TTATATATAC 1080  
 ATGCATGCAA GAGTTTGATA TGTATATTGT TTCATCATGG CTGAGTCAAA GTTTTATCCA 1140  
 AATATTTCOA TGGTGTGGTA TTAGTTAAAC AAATCTCTCG TATGTGTCAT TGAATATACC 1200  
 CGTGCATGTA CCAGGAATGT TTTTGATTCT AAAAACGTTT TTTTCTTTGT TGTAACGGTT 1260  
 GAGTTTTTTT CTTGTTTCA AAACGAGATT CTCGTTTGT TCTCCCTTG TCTAAAAACA 1320  
 TCTACGGTTC ATGTGATTCA AAAACACTAA AAAAATATAA ACTCATTTT TTTAATACT 1380  
 TAACATTTAA ACTATATATA TATATATATA TATATATATC TTATACTAGT CCCAAGTTT 1440  
 AGTGTGAGGT TTTTTATTCT AAAATCTATC AGTACATTTT TTGGAAAAGA ACTAAGTGAA 1500  
 ATTTTCTCCA AATTTTCCTT TTACTATTGA TTTTAAATT ACTGGATGTC ATTAACITTA 1560  
 ATCTTTTGAT TCTTTCAACG TTTACCATTG GGAACCTCA CATGAAATAA ATGTCTACTT 1620  
 TATTGAGTCA TACCTTCGTC AACATAAATT AATTGATGTT CTTCTCCAAA TTTTGAGTTT 1680  
 TTGGTTTTTC TAATAATCTT AACGAAAGCT TTTTGGTATA CATGTAAAAC GTAACGGCAA 1740  
 GAATCTGAAC AGTCTACTCA ACGGGGTCCA TAAGTCTAGA ATGTAGACCC CACAACTTA 1800  
 CTCTTATCTT ATTGGTCCGT AACTAAGAAC GTGTCCCTCT GATTCTCTTG TTTTCTTCTA 1860  
 ATTAATTCGT ATCCTACAAA TTTAATTATC ATTTCTACTT CAACTAATCT TTTTTATTT 1920  
 CCTAAAGATT TCAATTTCTC TCTGTATTTT CTATGAACAG AATTGAACTT GGACCAGCAC 1980

AGCAACAACC CAACCCCAAT GACCAGCTCA GTCATAGTAG CCGGCGCCGG TGACAAGAAC2040  
 AATGGTATCG TGGTCCAGCA GCAACCACCA TGTGTGGCTC GTGAGCAAGA CCAATACATG 2100  
 CCAATCGCAA ACGTCATAAG AATCATGCGT AAAACCTTAC CGTCTCACGC CAAAATCTCT 2160  
 GACGACGCCA AAGAAACGAT TCAAGAATGT GTCTCCGAGT ACATCAGCTT CGTGACCGGT 2220  
 GAAGCCAACG AGCGTTGCCA ACGTGAGCAA CGTAAGACCA TAACTGCTGA AGATATCCTT 2280  
 TGGGCTATGA GCAAGCTTGG GTTCGATAAC TACGTGGACC CCCTCACCGT GTTCATTAAC 2340  
 CGGTACCGTG AGATAGAGAC CGATCGTGGT TCTGCACTTA GAGGTGAGCC ACCGTCGTTG 2400  
 AGACAAACCT ATGGAGGAAA TGGTATTGGG TTTCACGGCC CATCTCATGG CCTACCTCCT 2460  
 CCGGGTCCTT ATGGTTATGG TATGTTGGAC CAATCCATGG TTATGGGAGG TGGTCGGTAC 2520  
 TACCAAAACG GGTCGTCGGG TCAAGATGAA TCCAGTGTTG GTGGTGGCTC TTCGTCCTCC 2580  
 ATTAACGGAA TGCCGGCTTT TGACCATTAT GGTCAGTATA AGTGAAGAAG GAGTTATTCT 2640  
 TCATTTTTAT ATCTATTCAA AACATGTGTT TCGATAGATA TTTTATTTT ATGTCTTATC 2700  
 AATAACATTT CTATATAATG TTGCTTCTT AAGGAAAAGT GTTGATGTC AATACTTTAT 2760  
 GAGAACTGA TTTATATATG CAAATGATTG AATCCAAACT GTTTTGTGGA TTAACTCTA 2820  
 TGCAACATTA TATATTTACA TGATCTAAAG GTTTTGTAAT TCAAAGCTG TCATAGTTAG 2880  
 AAGATAACTA AACATTGTAG TAACCAAGTT TAATTTACTT TTTTGAGTTT ACATAACTAA 2940  
 CCAAGCCAAA AGGTTATAAA ATCTAAATTC GTTGAGTTGT CAACTTCTG AAGATTGCTA 3000  
 TCCTCTTTGA GTTGCTTTCT TTTGGGTGCT TGAGTTTCAT TAGGCTGAGC TGAATCGTTG 3060  
 CTCTCTAGTC TTTCATCTCT GTCTTTTCCA AGGATTCATA ACGTTGGTCG CTCTCTGTTT 3120  
 CTGCTACAC TTCTTCAAGG GATCATTACT GAGGCTAAGA GTTAAAGACC TGAACCATGG 3180  
 TTTTCTGTAA CTGGTTCAAG TTCATTCTCC GGTATTGTG TGGTTATCTT TCGGTTAGAT 3240  
 TGAAACCCAT ATGTTTGCTC TGTTTCTTCT AGTTCCAAGT TTAATTTCCG GTTATTGTTT 3300  
 GGCTTTTTAA AAGTTTTTAA GGTCTATTCT ATGTAAAGAC TATTCTACGT ACGTACATTT 3360  
 ATCGCAAAAT TGAAAGATTA TAAAAAAAT TGAAA 3395

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7560 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATTNACCCT CACTAAAGGG AACAAAAGCT GGGTACCGGG CCCCCCTCG  
AGGTCGACGG 60

TATCGATAAG CTTGATATCG AATTCGTGGC CATTAGACCC ATAACTATAT  
GACGATGTTA 120

AAGAGAAAAT AAATCATAAA TAAAATAAGA GTCCTTATCA ATAAACCTAA  
TTGGCTAATT 180

TCAACCTCAA AGAGTAGTAG GAACAGGTAA GGTGAAGCCA AACAGCTCCT  
TTTACAGTTG 240

GACCACTAGA GCTGATCTGG CATACAAAGT ATGCTTATTG GGCTGTCACG  
GCCCATCCGC 300

AAAATGTCGT TGGTTACGAA GCATCCACGA CATAGACGGT GCCACATGTT  
AGAAAAGTGT 360

TTCGGCGATC AAGATTGTGT CCACATCATT AGACGTCTGA ACTGTCCACG  
TGTCTATCAA 420

AGCTGGCGTC AAACATTACG TTTTCGTCGT TTGCGCCTCC TAGTTCACAC  
GTGCAACGAA 480

CGCGTGCGAC GTATCAAAAT TGTTAATTTT AGCCATGTAT AAAGAATATC  
TACAAAATTA 540

ACCTCAGGAA TATTTTGTGTT TTTTCAATTG AGGCCATAAT ATACNTNCCG  
ATNGAAAAAT 600

TTTNCANCAT ATCNCTAATA TCAAAAAATT ATGATGTAG TAAACGTAAA  
AAATTTACAC 660

AAAATAANTT TCACAAAACCT TANNGGGGAA ATTGGAACAA ANAAAAGACT  
GGTGAGTGAT 720

AAGCGATGAT GGCCGGTGAA TCAGGTAGCC GTCCTACAAC GTGGTTGATT  
TTGAGCAAAC 780

TCCTATCTAC TCTTCACACT ATTGGAAATC CCAAATGTC GTCACACCAT  
AATAATGTGA 840

ATTTTGTTAT GGAATTTGAG GGAAACAGTA GATATATGTT TCAACCAGTG  
AAAGTTACCC 900

TCCTTTGGAC ATATCTACGA NAGTAGAAAG TAGAAACATT CACTAAACGT  
GACAACTTTA 960

TAAATTTTCT TTTTGTAAC TTTCTTTAGA TTTATTTACG ANAAGAGAAA  
TATAAACGTC 1020

ATGCTAATAA AAAATGCATT ATTTTCTACC ATCTAGCTAG AATATTGATC  
AAGTCTTCAC 1080

GTTTTTTGTT TATCTCTTCT CTCATAGGCA TGTCCACAAA AGGGTAAGTT  
TTACTGGTTC 1140

AAAATATTGC ATGAGTACTA CTAAGCTCGT ATAGTTTGAT CTTACTATCA  
TTGCGATGAG 1200

GGTTGTTAGT TTGGAAGAAA TAAGGATTTA TGCAAATGGT AATCATTATG  
TCTGCTATTT 1260

AAGAAGTAAA TTATGATGCT TGTTGCGTGA ACATATTAAA TTTGCGAAAA  
ATAAGCAAGG 1320

ATACACGAGA GAAGCTCAGA TATTCACGTA ACGATGTTTC ATCTCTTCTC  
ATTGAGGAAA 1380

CATATGGCCA TGATATAGCT AATAAGCCTA CGGGATTGTC NTTTCAACGC  
CGAATCTACC 1440

AAACTGTTCC ATCTCTTATT ATATATAGTT TGGTTATTTA AGTAATTAGA  
TGCATCATAA 1500

TCTTTTTTTC TGCCAGTTGT AATGCAGATA AAAATATATT GGTGTTCTA  
AGGATTGTTT 1560

AAACGTGCAT GTGTACAAGT TATTATTTAT ATACTTTCAT CTACATGCGA  
TGCGTTATTT 1620

ATAATGATAA AACTAAGATT TTTAGTTAAA TTTAATAAAG AGCTTACGAG  
CTACAATTAA 1680

TTAGAAATGG TTGCTCAGAA ATCAGAATAC TATATATGAA AAAAGAAGTT  
GGTATACTTG 1740

AAAAAAGAAA AAAC TACTTG AAAAGATGGT AAAAGATATA GAACGAGTAT  
ATATCTTACT 1800

CAAGCACGAT AGAAGTTTGT ATCAAAACAT TGC GTTCCAA ACCAATGTTT  
GAAGATGGTC 1860

AAAGGTGCTA CTCATGATGT GGTGCGAAGA AGCTTACGAA AAATTCTGCA  
ATGAGAGATA 1920



ACTTTATGGG CTGCTTGTTT AATATATTGA AAATCATGGT AGACAACACC  
AAACTCTCCT 1980

TTACCAGAAG TCATATTTCC TTAACCTCAG AATAAGTAAA TCTTCTAGTT  
TATTATTTGA 2040

AAGTTGAGCG TATAATTGCA ATGAACTTT TACCAATTCA CCGCCTCCTA  
ACTGAGTTGT 2100

TGTATTATCC TATCTCTTTA GCTATCCTTT CCTTGCTCTT GCTCCACCTG  
CATGTGGCCT 2160

CTTTATTTAT AATCTCTCTA GATTCTGCTA AAGATGTNTG TTCAAAATGG  
TTATCTTTA 2220

AGGGAAGCAA AGTGAATGGA AACATTTAAA GAAAAAAAAA ACTTTTAGCA  
GAGTTCCATG 2280

AGATTTTATA CTGATGATAA CTAAAATAAT CTTATATGCG TAAGATTATT  
TTAGTTCTAA 2340

ACTTCATTTT GAAATGAGAG GTCATTGGCC AGGAAAGATT CAATATTGGT  
TCTTTGTAA 2400

TTCTCGTTGG TTGTGTTTTA GTATGGGCTA GATCCAAAAC AGGTCATGGA  
CTGGGCCGTA 2460

AACTCTATCC AAAATTCTTC ATGTTTTTCC ATCTTTCAA AATCTTTATC  
CACCATTCCA 2520

TTACTAGGGT GTTGGTTTTA TTTTATTGT TGATTAATTA TGTATTAGAA  
AATGTAAAGC 2580

AATATTCAAT TGTAACATGC ATCATCTAAC ACCAATATCT TGTACTAACC  
TTTTGTAAAT 2640

TTCCTATAAA CATTTTAAAA GGCTAATTTA AATAAAAATT ACAATAAACG  
TGATAACTCA 2700

CTTTCGTAAC GCATATTTAT TCAAATATAC CAAAATTAC CATTTTAAGT  
AAGAGAATCT 2760

TTTTAAAATT AATTTTCAAT TTCATTAATT AAGAAACAAA GAATTTACTG  
AAACCTATAT 2820

TTTATTAAAT TTTAATAAAA TATATGACTA AAATAACGTC ACGTGAATCT  
TTCTCAGCCG 2880

TTCGATAATC GAATACTTTA TTGACTAAGT ATTTATTTAG AAAATTTTAA  
ACAACACTTA 2940

ATTTCTAGAA ACAAAGAGAG CCTCATATGT ATAAAAATCT TCTTCTTATC  
TTTCTTTCTT 3000

TCTTAATAGT CTTTATTTTT ACTTAATTAC TTTGGTAATT TGTGAAAAAC  
ACAACCAATG 3060

AGAGAAGAGC AGTTTGACTG GCCACATAGC CAATGAGACA AGCCAATGGG  
AAAGAGATAT 3120

AGAGACCTCG TAAGAACCGC TCCTTTGCCA TTTGTATCAT CTCTCTATAA  
AACCCTCAA 3180

CCATCAACCT NTCTTTGCAT GCAACAAATC ACTCAAATAA TTATTTTATA  
AAGAACAAAA 3240

AAAAAAGAC GGCAGAGAAA CAATGGAACG TGGAGCTCCC TTCTCTCACT  
ATCAGCTACC 3300

CAAATCCATC TCTGGTAATC TAAGTGGCTA TTTGTATACA GTATATACTT  
GCCTCCATGT 3360

ATATTTATAT TCTCGTGAAA AATTGGAGAC ATGCTTTATG AATTTTATGA  
GACTTTGCAA 3420

CAACGAACGA GATGCTTTCT CTCTAGAAAT TTAAATTTAG ATTTGTGAAG  
GTTTTGGGAA 3480

TGGCCCGGAG AAGACGATTT TATATATACA TGCATGCAAG AGTTTGATAT  
GTATATTGTT 3540

TCATCATGGC TGAGTCAAAG TTTTATCCAA ATATTTCAT GGTGTGGTAT  
TAGTTAAACA 3600

AATCTCTCGT ATGTGTCATT GAATATACCC GTGCATGTAC CAGGAATGTT  
TTTGATTCTA 3660

AAAACGTTTT TTTCTTTGTT GTAACGGTTG AGTTTTTTTC TTCGTTTCAA  
AACGAGATTC 3720

TCGTTTGTCT CTTCCCTTGT CTAAAAACAT CTACGGTTCA TGTGATTCAA  
AAACACTAAA 3780

AAAATATAAA CTCATTTTTT TTTAATACTT AACATTTAAA CTATATATAT  
ATATATATAT 3840

ATATATATCT TATACTAGTC CCAAGTTTGA GTGTGAGGTT TTTTATTCA  
AAATCTATCA 3900

GTACATTTTT TGGAAAAGAA CTAAGTGAAA TTTTCTCCAA ATTTTCCTTT  
TACTATTGAT 3960

TTTTTAATTA CTGGATGTCA TTAAC TTAA TCTTTTGATT CTTTCAACGT  
TTACCATTGG 4020

GAACCTTCAC ATGAAATAAA TGTCTACTTT ATTGAGTCAT ACCTTCGTCA  
ACATAAATTA 4080

ATTGATGTTT TTCTCCAAAT TTTGAGTTTT TGGTTTTTCT AATAATCTTA  
ACGAAAGCTT 4140

TTTGGTATAC ATGTAAAACG TAACGGCAAG AATCTGAACA GTCTACTCAA  
CGGGGTCCAT 4200

AAGTCTAGAA TGTAGACCCC ACAAACTTAC TCTTATCTTA TTGGTCCGTA  
ACTAAGAACG 4260

TGTCCCTCTG ATTCTCTTGT TTTCTTCTAA TTAATTCGTA TCCTACAAAT  
TTAATTATCA 4320

TTTCTACTTC AACTAATCTT TTTTATTTC CTAAAGATT CAATTCTCT  
CTGTATTTTC 4380

TATGAACAGA ATTGAACTTG GACCAGCACA GCAACAACCC AACCCCAATG  
ACCAGCTCAG 4440

TCATAGTAGC CGGCGCCGGT GACAAGAACA ATGGTATCGT GGTCCAGCAG  
CAACCACCAT 4500

GTGTGGCTCG TGAGCAAGAC CAATACATGC CAATCGCAA CGTCATAAGA  
ATCATGCGTA 4560

AAACCTTACC GTCTCACGCC AAAATCTCTG ACGACGCCAA AGAAACGATT  
CAAGAATGTG 4620

TCTCCGAGTA CATCAGCTTC GTGACCGGTG AAGCCAACGA GCGTTGCCAA  
CGTGAGCAAC 4680

GTAAGACCAT AACTGCTGAA GATATCCTTT GGGCTATGAG CAAGCTTGGG  
TTCGATAACT 4740

ACGTGGACCC CCTCACCGTG TTCATTAACC GGTACCGTGA GATAGAGACC  
GATCGTGGTT 4800

CTGCACTTAG AGGTGAGCCA CCGTCGTTGA GACAAACCTA TGGAGGAAAT  
GGTATTGGGT 4860

TTCACGGCCC ATCTCATGGC CTACCTCCTC CGGGTCCTTA TGGTTATGGT  
ATGTTGGACC 4920

AATCCATGGT TATGGGAGGT GGTCGGTACT ACCAAAACGG GTCGTCGGGT  
CAAGATGAAT 4980

CCAGTGTGG TGGTGGCTCT TCGTCTTCCA TTAACGGAAT GCCGGCTTTT  
GACCATTATG 5040

GTCAGTATAA GTGAAGAAGG AGTTATTCTT CATTTTTATA TCTATTCAA  
ACATGTGTTT 5100

CGATAGATAT TTTATTTTTA TGTCTTATCA ATAACATTTC TATATAATGT  
TGCTTCTTTA 5160

AGGAAAAGTG TTGTATGTCA ATACTTTATG AGAAACTGAT TTATATATGC  
AAATGATTGA 5220

ATCCAAACTG TTTTGTGGAT TAAACTCTAT GCAACATTAT ATATTTACAT  
GATCTAAAGG 5280

TTTTGTAATT CAAAAGCTGT CATAGTTAGA AGATAACTAA ACATTGTAGT  
AACCAAGTTT 5340

AATTTACTTT TTTGAGTTTA CATAACTAAC CAAGCCAAAA GGTATAAAA  
TCTAAATTCG 5400

TTGAGTTGTC AAACTTCTGA AGATTGCTAT CCTCTTTGAG TTGCTTTCTT  
TTGGGTGCTT 5460

GAGTTTCATT AGGCTGAGCT GACTCGTTGC TCTCTAGTCT TTCATCTCTG  
TCTTTTCCAA 5520

GGATTCATAA CGTTGGTCGC TCTCTGTTTC TGCCTACACT TCTTCAAGGG  
ATCATTACTG 5580

AGGCTAAGAG TTAAAGACCT GAACCATGGT TTTCTGTAAC TGGTTCAAGT  
TCATTCTCCG 5640

GTTATTGTGT GGTTATCTTT CGGTTAGATT GAAACCCATA TGTTTGCTCT  
GTTTCTTCTA 5700

GTTCCAAGTT TAATTTCCGG TTATTGTTTG GCTTTTTAAA AGTTTTTAAG  
GTCTATTCTA 5760

TGTAAAGACT ATTCTACGTA CGTACATTTA TCGCAAAATT GAAAGATTAT  
AAAAAAAATT 5820

GAAAGATCCA AAGGAAACCA ATAGATTAAA CTAAAATGTA GTATCCTTTT  
TATCATTTTA 5880

GGCTATGTTT TCTTTTAAGA AAGCTTTGGT AGTTAACTCT GTTTAAAAGA  
AAAAAAAGAG 5940

ATGCATAAAT TAAATTTAAG TTTCTAGAAC TTTTGGATAA ACATATTAAG  
CTAAAGAAAT 6000

TAAACTAAAG GGCGTAAATG CAAGCTTGTT ATGCGTTATT GAAAACATTA  
CCTCTAAATT 6060

AAATAGCCCA ATATTGAAAA CCTTAAGCTT CTTTGATCCC CTTAACTTGT  
TTGTCCACCA 6120

AGTATTAGTT CATCTCTTAA CACGGCAACT CGAAACGGCA CAATGGACAA  
ACATGGTCTT 6180

TCAAAAACCA CTTCCCAATA CATCCATCGT CAAACTCGTG GCCACATGGT  
AAGGTCACCA 6240

CTATTTCTCC CTTTTCAAAC TCCTCCAAAC AAATTGTGCA CAACTGGCG  
TCAGAGTTGG 6300

ATTTCTTCTT ATTATTATAT ACTTTCCTTG CCAAACGGTC AACCACAAAC  
TTATTTGCCG 6360

GTCTAATTAA CTCGATATTA TTGGTGGTCT CATCAAACGA GTCAATCCGA  
GGAGGAGGTG 6420

GAACAATGAC TTTACAGTAC ATGTAAACTA ACGTAGCACA AACTGAAGAG  
TCTACCATAG 6480

AAATCGACTT ACAGATTCGT TCAGTGAGTT GAGAGTTAGC AATGTCAACA  
TATTGTTCGG 6540

AGAGCCCTGC TGAGTACAAC CATTCAATCA GTTTTTTCGA GTCATTAGGG  
TAGGAGGATA 6600

TGACACCTTC GTAGTCATTG TACGAGAGAA CGAAATTTGG TGGAAGACTA  
ATTGATGTGT 6660

CCGATCTTCG GGCACCTACG CAGATTTTGA ATGATCCAGC ATCTTGTGAT  
TTCGGTTTGA 6720

GGTCTATTTT GCCGCCAAAG GATATTTCCG CTTCCATAGC TATCAAAGAG  
AAAGAAAAAT 6780

AGTGAATCCA AGGTTTAGGG TTTCTTTTCT TTGTCTTCT TATATATAGA  
GGCGCTAGAT 6840

TGTATTAAGG ATTATACATA TATATAAGTA ATTGCAATTT GTGAGTTTAT  
CCTTATTCAT 6900

TTTTAATTTT ATTTACCTTT ATTTAGTTGA TATTGTGTCC TTTTCCTAGG  
TAGCATTTC 6960

TTCCATCTGT GTTAATTATT AGCATTTCCT TTCCTTTGTC TTATTTGCCT  
TTATTTTCGTA 7020

GGAAGAAATC CTTTATGNAC CCCATCTTGG CTGAGAACTT GAGATGATTT  
TAAATCCTCA 7080

AAAATTATTC AATTTATGAT TTCGAAATTG ATATACACTT TATATTTTCT  
CCTAAAAAAC 7140

CATATTGTAC TAAGAAAAGT AGAAAACCAG ACTTTTAAAT ATGTTAGATT  
TTAATTGGGT 7200

TCTTAAAGTG TTTTAGCGTT TNACACCGGT TATTCTCAA AATCCAACT  
CTATAATTAT 7260

AGTTTTTAAG TATAAATTAA TCCGGTGGC CCAATTAGTG GACCGTTTAA  
AGAGTAGACA 7320

CTTTTTTTTT TATATATCGA CTACCATAAA ACTTTAACGA TTAATATTTT  
TGGATAATAA 7380

GCGATCGTTT TGAGGCGTCC CAATTTTTTT TGTTTCTTTT TATATGAGAA  
ATGGGTTTAA 7440

GAAAAACTGC AATTTTGTCC ATAAAGCTAG TCAGAATTCC TGCAGCCCCGG  
GGGATCCACT 7500

AGTTCTAGAG CGGCCGCCAC CGCGGTGGAG CTCCAATTCG CCCTATAGTG  
AGTCGTATTA 7560

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Pro Ile Ala Asn Val Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGAATTCAGC AACAAACCCAA CCCC

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTCTAGACA TACAACACTT TTCCTTA

27

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGACCAGCT CAGTCATAGT AGC

23

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCACACATG GTGGTTGCTG CTG

23

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGATAGAGA CCGATCGTGG TTC

23

## (2) INFORMATION FOR SEQ ID NO:12:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCACTTATAC TGACCATAAT GGTC

24

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCATAGATGC ACTCGAAATC AGCC

24

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTTGGTAAT AATTGTCATT AG

22

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTAAAAACAT CTACGGTTCA

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTGTGGTTG ACCGTTTGGC

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Pro Ile Ala Asn Val Ala  
1           5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val  
1            5            10

SEQ ID NO:19: *Arabidopsis* L1L gene (pMNJ7 sequence)

ATGGCAGAGG GCAGTATGCG TCCTCCAGAA TTCAACCAGC CTAACAAAAC  
CAGTAATGGT GGTGAGGAGG AGTGCACGGT GAGGGAGCAA GACAGGTTCA  
TGCCTATTGC CAACGTGATA CGGATCATGC GGAGGATCTT ACCTGCTCAC  
GCCAAGATCT CAGATGACTC CAAGGAGACG ATCCAAGAGT GTGTTTCGGA  
GTACATCAGC TTCATAACAG GGGAGGCTAA TGAGCGGTGC CAGCGGGAAC  
AGCGCAAGAC CATCACTGCT GAGGACGTCT TGTGGGCAAT GAGCAAGCTC  
GGTTTTGATG ACTACATCGA ACCCCTCACG TTGTACCTCC ACCGCTACAG  
AGAGTTGGAA GGTGAAAGAG GGGTTAGCTG CAGTGCTGGG TCCGTTAGTA  
TGACCAACGG CTTGGTGGTC AAGAGGCTTA ATGGGACCAT GACCGAGTAT  
GGAGCCTACG GGCCTGTGCC AGGGATTAC ATGGCGCAGT ACCATTATCG  
TCATCAGAAC GGGTTTGTTC TCAGTGGTAA CGAACCTAAT TCTAAGATGA  
GTGGTTCATC TTCAGGAGCA AGTGGCGCCA GAGTTGAAGT ATTTCCGACT  
CAACAACATA AGTACTGA

SEQ ID NO:20: *Arabidopsis* L1L protein

MAEGSMRPPE FNQPNKTSNG GEEECTVREQ DFFMPIANVI FIMPRILPAH  
AKISDDSKET IQECVSEYIS FITGEANERC QREQEKTITA EDVLWAMSHL  
GFDDYIEPLT LYLHFYFELE GERGVSCSAG SVSMTNGLVV FRPHGTMTVEY  
GATGPVFGIH MAQYHYEHQN GFVFSCHIEFN SKMSGSSSGA SGARVEVFPT  
QQHKY

SEQ ID NO:21: *Phaseolus* gene

GATCTCTCAACCCAACCCTTTCATTTTCATTTTCATTTTCATTTTCCATCACTTCACTGTC  
ACCATGGAAAG  
TGAGAGCTTTCATGGCTACCGCAAGCTCCCAACACCACCTCTCCTGGGTTGAAGCTGTCAG  
TCTCAGACATG  
AACAACGTGAACACGAGTAGGCAGGTAGCAGGAGACAACAACCACACAGCGGATGAGAGCAA  
CGAATGCACTG  
TGAGGGAGCAAGACCGTTTCATGCCAATTGCAAATGTGATCAGGATCATGCCAAAGATTCTT  
CCTCCACATGC  
CAAGATCTCAGGTGATGCCAAAGAAACAATTCAAGAGTGTGTGTCTGAGTACATCAGCTTTA  
TCACCGGAGAG  
GCCAAACGAGCGTTGCCAGAGGGAACAACGCAAGACCATAACTGCTGAGGACGTGCTTTGGGC  
CATGAGCAAGC

TTGGATTTGATGATTACATGGAGCCACTGACCATGTACCTTCACAGGTATCGTGAGCTTGAG  
 GGTGACCGAAC  
 CTCATGAGAGGTGAATCATTGGGSAAGAGGACTATTGAATACGCCCCATATGGGTGTTGGCG  
 TTGCTACTGCT  
 TTTGTGCCACCACAGTTTCACCCAAATGGATACTATGGTCCTGCCATGGGAGCTTACGTTGC  
 GCCACCAAATG  
 CTGCGTCTCTCATCACCATGGAATGCCAAATACTGAACCGAATGCTCGCTCCATGTGAATT  
 GATGATGATGA  
 GGAGGAGGAGGAGGAAGACGACGASTGTTGASTTAGTAGAAGAAGAATACTTTAATTAATTA  
 GCTTAACCTCTC  
 GGTAAATTAGAGTACTGTTGTTGAGGGTACGTAGTAAACTTTATAATTAAGGGGATGGATGGG  
 ATTAAGGAGTT  
 CTGATATTCCTAATCCTAATCAGGCCTATGTTAATTTATGTAATAACTCTGCTTATGTTTTT  
 GGATTTTCTGA  
 TGTGTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO:22: *Phaseolus* protein

MESGGFHHGYRKLPHNTTSPGLHLVSVDMMNNVITSPQVAGENNNHTADESNETTVREQDREMPIA  
 NVIFIMRKILP  
 PHAKISGDAKETIQECVSEYISFITGEANERCQREQFKTITAEVLWAMSKLGFDDYMEPLT  
 MYLHPYRELEG  
 DETSMEGESLGRHTIEYAPMGVGVATAFVFPQFHPNGIYGPAMGAYVAFPNAAASSHHHGMPN  
 TEPNARSM

SEQ ID NO:23: 5' untranslated region

atgatttctct	tctctctctt	caaatggagt	tttaagctng	ttggttttca	aaggaagag
gtctctctct	caggtataaa	tctcaccatt	aaaaatctga	gttttttctt	caatttggga
tctgttaactg	tgaaaagttg	ttactttttt	tctgtattat	taagagctta	atttttttct
aggttaatta	gaagotttgt	tggttagagac	ctctataaaa	cattctctct	ctcttgatat
atttgaatt	tgggttatca	tctgacttca	gatttggttg	cttggtgctc	actgaacat
ctcagcttaa	agcattaaac	tctgcagata	tcaatagat	tctgttgccg	tcattataag
cttttaacgt	gttggtttat	accacttcta	agcagtggtt	gtctatatat	tctggtgaac
tttttgatta	ttagtcttta	gatagtgtaa	ccatgttgga	agctttgagt	ttttgataag
taatttcaaa	tttttgattt	tgcagctcct	ctgttgatag	cagcgatagt	gaotcctctc
cagagtttct	caagaccjtc	acgggtaaaa	gaaagcggga	aacaaggjta	aaactgganc
atttttttga	gaagotttgt	gggagtatga	tgaagcggga	ggagaagatg	cataatcagt
tqattaatgt	gatggagaag	atgggaagtgt	agagaataaa	ccctgagga	gcttggagtc
aacaggaac	cgaaaggatg	acacagaatg	aaagagcaag	aaagcaagag	atgacacaa
acttctctct	cattctctct	atcagaagtgt	ttactgttga	agagatcttg	actctaaac
agtggtgaatt	cttgcaacca	ctcragcaga	ttcttctgga	agaatctaa	gcttgaat
gttaattctg	ttaagagagaa	agagagatga	acttttagjta	ctcaagcggc	actggagga
gttggtgaag	gggtccgcaa	gaggaagtgc	agacattgat	acttttagga	agcagatctg
aaagaaagac	gggtatcaac	aaaggagaga	tttgggtatga	gatatagga	agaatgaag
aaagagggtta	cgaaaagatct	gggaagaaat	gttaggagaa	gttggaac	atgaacaa
actataggaag	agtgaacgaa	ggtgggagga	aaagcctga	actatagaa	actggtctct
actttgagaa	acttggaat	ttttacaaga	caatttctct	gggagagag	gaaatctgag
tgaagattct	taaatttagg	gttttttggc	acgcaaaaag	ggagaacttg	taagtgtat
ctctgagttt	aaattttata	cttttgggtgt	agtttatat	ttaaaactct	actgtctgt
atttggagaa	ggttogaata	aaaaagacaa	atacgttggg	gtgattggga	tttggagag
gctaagcgag	acjaggagaa	ggatcctcgg	tcacatcgat	tatggtctgc	actgtttga
acttjtgagg	tctgaaatta	caaatgtgtg	caattgcaaa	cactattagc	ttttctcaa
ttactctctc	ttctctctca	ttcactctct	ttcttcaaat	gotttctaat	tttgggtatt
ggttattatt	atttataggg	atattcacia	acacaaaagt	ggttatatta	gaacaagaaa

gatatggaac gtggaggett ccattggetac cgcagctgt cegtgaacaa caccactcct  
tctccaccag gtatggcat tctctatacc cctctcttcc acaggetctc ttcatttcag  
ttgcattgga aaccattctc tgcaatccct ccattgtcat gtctgtactc ttttcattgac  
gaacagttaa tgaaatagct tttcaatctt ataaaccgag catgcagacg tcatcgaagc  
cattatgcac taaaacttcc attttcttta tttttgttag gatttagcagc gaattttctg

# SEQ ID NO:24: 3' untranslated region

ga acaatggcta ataacataga cagctgacag agtcataaet  
gttagtaggt gcaagctgtc gcttatgaat tcaagtttaa gcgaaaaaaa tgcctgtttt  
tctttgttta ttatctatct agttgaaaga acattgtgtt tttcatctga tctgtcttgt  
ggtaaagtat gtaataaag cattagtttt gaaaccgca tgcattgtat attacaaaat  
tcacggtgaa ttctgaatgc gtcttggttc aaaaatagaa gagactaaac attccagatt  
tcaattctca gctacagaaa tgagtgttta acggatacag aaacaactct cacaatcttc  
attcatttca tttagctact actttccaaa ggaacttcaa cgcatacctt tttcctctcc  
agaagatcat gtttgtctgc actctcgttt gctcagat ctctctctg atgctcttca  
gatatagtt ccaatttcga acaatcaaca gcatcaagtc cgttctttt cctctgagga  
atcacagtga agaaggtgt tttccagtc ctactctca gaaacttgac gactatctcc  
aaaacttqgt tcacagtga aacctaaatc aataaaaaac acaaatctta cattaacaaa  
gtacataaag tagaggtttt ttgtgtgtg cccaatgaga caagaattga agtggccatt  
tagttacctg agaacttgac attttcatat actctctat gggaagctta gctgttttaa  
tgcttggtc ttgagccttg gtcattgtga tcccttgaa ccggtttcga tccactaagc  
cacggataat gtagatatgc ttagggtcaa gatcctcaa aacagtttca gaatcagcgc  
taagatacac caaattatct ttctgatcag ccattggttc aatgtaaac ctactttct  
tttcaatgaa ccatttctca aaaccaggaa gcttgtaag ctactactc atcttccc